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OM protein - protein search, using sw model

Run on: June 23, 2003, 08:31:36; Search time 41.0409 Seconds (without alignments)
431.003 Million cell updates/sec

Title: Perfect score: Sequence: US-10-077-137-1 964 1 MLQMAGQCSQNEYFDSLLHA......CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

earched:

283224 seqs, 96134422 residues

ll number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : pIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	6	51	4) ω	N	_	Result No.
73	73	73.5	73.5	74	74.5	74.5	75	75	75.5	76	76	76.5	76.5	77	77	77.5	77.5	78	78.5	79.5	79.5	81	81.5	82	83.5	g	88.5	964	Score
7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.8	7.8	7.8	7.9	7.9	7.9	•	8.0	. 8.0	•	•	8.1	8.1	8.2	8.2	8.4	8.5		8.7	9.0	9.2	100.0	Query Match
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	hypothetical prote	conserved hypothet	membrane protein [a		ERD1 protein - yea	S-receptor kinase	hydrogenase chain	probable transcrip	complex I intermed	sialo	_	hypothetical prote	rt			hypothetical prote	killer cell inhibi	potassium channel	furin (EC 3.4.21.7	•	R08F11.7	surface protein 51	protein-tyrosine k	hypothetical prote	prominin - mouse	amino acid ABC tra	tio	Description

444	421	49 0	38	36 37	S	υ ω	32	31	30
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7.3	7.4	7.4 7.4	7.4	7.4	7.4	7.5 n	7.5	7.5	7.6
412 424	500	473 480	414	62 7 22 7	105	416	408	243	733
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hypothetical prote S-locus-specific g	hypothetical prote spike glycoprotein	ABC transporters (protein F41H10.1 [probable cell divi	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	probable serine/th

ALIGNMENTS

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Qy Db	D Q	da Vo	Query M Best Lo Matches	A;Cross-ref C;Genetics: A;Gene: GDB A;Cross-ref A;Map positr A;Introns: C;Superfami	A; Molecule A; Residues: A; Cross-ref A; Accession A; Status: p A; Molecule A; Residues:	A;Statu A;Moleci A;Resid A;Cross R;Laabi EMBO J. A;Tefte A;Access	RESULT 1 \$43486 B-cell matur. N,Alternate C;Species: H C;Date: 27-J C;Accession: R;Laabi, Y; R,Laabi, Y; Nucleic Acid. A;Title: The A;Accession: A;Accession:
121 YTVEBCTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180 	61 GLSLIISLAVFVLMFLLRKISSEPLKDBFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120 	1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA:	Query Match 100.0%; Score 964; DB 2; Length 184; Best Local Similarity 100.0%; Pred. No. 5.6e-81; Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Cross-references: EMBL:Z14955 C;Genetics: A;Gene: GDB:BCMA A;Cross-references: GDB:135977; OMIM:109545 A;Map position: 16p13.1-16p13.1 A;Introns: 44/1; 93/1 C;Superfamily: human B-cell maturation factor	A;Molecule type: mRNA A;Residues: 1-184 <la2> A;Residues: 1-184 <la2> A;Cross-references: EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:g29408 A;Accession: S36661 A;Status: preliminary A;Status: preliminary A;Molecule type: mRNA</la2></la2>	A;Status: preliminary A;Molecule type: DNA A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245 A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245 A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;10) A;Reference number: S31208; MUID:93010984; PMID:1396583 A;Accession: S31208	RESULT 1 \$43486 \$43486 \$640 maturation factor - human B-cell maturation, is bidire B-cell maturation, is bidire

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C;Species: Clostridium acetoDuty11cum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_c
C;Acciession: C97344
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K
R; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genomber A;803-4838, 2001
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97344
                                                                                                                                      A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-858 «WEI">A;Crose-references: EMBI:AF026269; A;Experimental source: kidney C;Keywords: glycoprotein; membrane
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Best Local S
Matches 55
                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                        Species: Mus musculus (house mouse)
Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
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                                                                      Matches
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                                                                    30;
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                                                                                       Score 86.5;
Pred. No. 6
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                                                                                                      Length 858;
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A;Accession: A....
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1009 <SAS>
A;Cross-references: GB:D45854; NID:g1000679; PIDN:BAA08290.1; //
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kina
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase
C;Keywords: ATP; phosphotransferase; tyrosine-specific proteir
C;Keywords: ATP; phosphotransferase; tyrosine-specific proteir
C:423-686/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A57434
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J. Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta,
A;Reference number: A57434; MUID:95403356; PMID:7673154
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A;Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; C;Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1998 <CHO>
A;Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20
A;Experimental source: cultivar Columbia; BAC clone T24C20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T24C20.80 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change C;Accession: T13009
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A;Accession: T13009
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Query Match
Best Local Similarity
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Pred. No. 2
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82;
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18;
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C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
                                                                                                                                                  A; Cross-references: GB:chr_V;
A; Note: Similar to peroxidase
                                                                                                                                                                                                                                                A;Title: Genome sequence of the nematode C. elegans: a platform for investigating A;Reference number: A75000; MUID:9965613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 199
                                                                                                                                                                                                                                                                                                               C;Accession: D89010
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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A;Molecule type: DNA
A;Residues: 1-2233 <NIE>
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                                                                                   Map position:
Superfamily:
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pecies: Caenorhabditis elegans
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Cross-references: EMBL:M65164; NID:g159974; PID:g159975; PIDN:AAA61740.1
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Best Local :
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Mol. Biol. 222, 835-841, 1991
Lie: Cystedine residue periodicity is a conserved structural feature of variable surf ference number: Z20504; MUID:92106337; PMID:1762150
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25.1%; Pred
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fall armyworm
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R;Lev, S.; Moreno, H.; Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.; Plowman, G. Nature 376, 737-745, 1995
A;Title: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion chann A;Reference number: 860248; MUID:95379967; PMID:7544443
A;Accession: S60248
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A;Residues: 1-22,'G',24-434,'L',436-1009 <SAS>
A;Residues: 1-22,'G',24-434,'L',436-1009 <SAS>
A;Residues: 1-22,'G',24-434,'L',436-1009 <SAS>
A;Residues: 1-22,'G',24-434,'L',435-21,'ND:g1165218,'PIDN:AAC05330.1; PID:g1165219
A;Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1915
A;Title: Cloning and characteriztion of cell adhesion kinase beta, a novel pa;Reference number: A57434; MUID:95403356; PMID:7673154
A;Accession: B57434
                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase F;423-686/Jomain: protein kinase homology <KIN>F;431-439/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884; PID:g1000677
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A; Residues: 1-22, 'G', 24-150 <SA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1009 <LEV>
A;Cross-references: EMBL:U33284; NID:g988304; PIDN:AAC50203.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 10-Apr-1996 #sequence_revision 27-Feb-1997 #text_change 17-Nov-2000 C;Accession: S60248; G02330; B57434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine kinase (EC 2.7.1.112) CAK-beta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
                                                                139 DSDHCFPLPAMEEGATIL 156
                                                                                                                             KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI
                                                                                                                                                                                              EFKNTGSGLLGMANIDLEKSR ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRNTSVTGSPLPSTRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA
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                                                                                                                                                                                                                                                           Conservative |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ
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BEGOAVL
                                                                                                                                                                                                                                                                                      8.2%;
320
                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                          Score 79.5;
Pred. No. 31
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                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                           TGDEILLPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                                                                                                                                     Length 1009;
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N;Alternate name
C;Species: Spod
C;Date: 11-Jan-
C;Accession: T4
R;Cieplik, M.;
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                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Residues: 1-1299 <CIE>;Cross-references: EMBL;Z68888; NID:g1167859; PID:e219690; PIDN:CAA93116.
;Cross-references: chone Sfurin 6; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; species: Spedoptera frugiperda (fall armyworm)
10ate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
10acession: T43251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-343 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:U67575; GB:L77117; NID:g1591992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tatus: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccession: D64469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   position: REV1308326-1307295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1206 GALHTAPSADAAPSVAVVTIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                   141
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                                                                                                                                                                                                                                                                                                                                          12
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Similarity 24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                      EYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVF
                                DVLKEEYEKYPDKFLYIVGDAKKEEVLK-KAKIDKAKGLIATLPSDADNVFLTLTARELN
                                                                                          EII-----LPRGLEYTVEECTCEDCIKSKPKV------
                                                                                                                                                        IAEFIVEGKFEEFVRLKKMKNKIKTLKDHYIICGYGRLGKVVGEKFIEENIPFIAIDINE
                                                                                                                                                                                                                  VLMFL-----LRKISS--EPLKDEFKNTGSGLLGMA-----NIDLEKSRTGD
                                                                                                                                                                                                                                                                               DYFTALYFSVI------TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VEYSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDSDH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAGKRRIAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein sll0993
                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 78.5; D
; Pred. No. 13;
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Mismatches
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LTSCTDQEGPVEYEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:AAB99365.1; PID:g1592000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1289
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                                                                                          DSDHCF-PLPAMEEG
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dek, A.
                                                                                                                                                    C;Accession: D86345

C;Accession: D86345

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
D86345
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F;24-941/Product: killer cell inhibitory receptor p91A #status predicted <MAT>
F;24-118,119-220,221-315,316-448,419-517,518-618/Domain: extracellular Ig-like
F;636-674/Domain: transmembrane #status predicted <TMM>
F;675-765/Domain: cytoplasmic #status predicted <CYT>
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A;Accession: JC5894
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
JC5894
Killer cell inhibitory receptor p91A precursor - mouse C;Species: Mus musculus (house mouse)
C;Date: 18-Mar_1998 #sequence_revision 18-Mar_1998 #te:
A;Cross-references: GB:AE005172; NID:g8920639; PIDN:AAF81361.1; C;Genetics:
                                                          A; Molecule type: DNA
A; Residues: 1-738 <STO>
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J. Biochem. 123, 358-368; 1998
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                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comment: This protein function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LEYTVEECTCEDCIK----SKPKVDSDHCFPLPAMEEGATILVTTKTN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 78; DB 22.7%; Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                GSPDB:GN00141
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T01733
A;Map position: 3
A;Introns: 69/3; 271/3;
A;Note: F2K15.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot
                                                                                                                                                                             A; Reference number: Z23015
A; Accession: T45824
                                                                                                                                                                                                                                                                                                                                          T45824
                                                                                                   A;Cross-references:
                                                                                                                   A;Residues: 1-522 <RIE>
                                                                                                                                                                                                                                                                    hypothetical protein F2K15.50 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                              A;Experimental source: cultivar
                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191152
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                            ;Rieger, M.; Gabel, C.;
ubmitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: DNA
;Residues: 1-968 <SCH>
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;Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3;
;Note: A_IG002N01.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: translated from GB/EMBL/DDBJ
                                                           Genetics:
                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                          Accession: T45824
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Best Local (
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pecies: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                       M.; Gabel, C.; Mueller-Auer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAMEEGATILVTTKTND----YCKSLPAALSATEIEKSISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELKEIGKAL-
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                                                                                               EMBL: AL132956
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                    294/1; 327/3; 397/3; 443/3
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26.2%; Pred. No. 34;
ative 21; Mismatches 45;
                                                                                                                                                                                                                  Sequence
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                                                                          Columbia; BAC clone F2K15
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Pred. No. 45;
                                                                                                                                                                                                                  Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                  S.; Schaefer, M.;
base, January 2000
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                                                                                                                                                                                                                                 Zipp,
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                                                                                                                                                                                                                                   M.; Mewes, H.W.;
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                                                                                                                                                                                                                                                                                                                       A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein
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A;Molecule type: DNA
A;Residues: 1-539 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methyl-accepting chemotaxis protein - C;Species: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A72200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 11-Jun-1999
                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                    ;Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36222.1; PID:g498169;
Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: F72288
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Best Local (
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completed: June 23, ne : 44.0409 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evidence for lateral gene transfer between Archaea and Bacteria ce number: A72200; MUID:99287316; PMID:10360571
                                                                               203
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                                                                                                                                                                                                     42 NASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD---EFKNTGSGLLG
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                                                                                                                                                             NVSMTKNIK-RNIIFF----LVVVCABAMFIAIFTTRNLTT-PLKKLAVLVENLSHGVL-
                                                                                  --NVEIEKIRSKDEI
                                                                                                                   MANIDLEKSRTGDEI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLVLACMRKTSNPDELPSLPYQYRSSSRSSLLTTGSRSDSRLLWLVK----VIWTAVILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLHAC-----IPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTC--LG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                             8.0%; Score 77; DB 2; Length 539; 32.0%; Pred. No. 28; tive 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 77; DB 27.0%; Pred. No. 27; tive 18; Mismatches
                  2003;
                                                                                  215
                     08:40:13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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